

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 23:19:26 ; Search time 26 Seconds
(without alignments)
1564.478 Million cell updates/sec

Perfect score: 2527
Sequence: 1 MVKFPALHYWFLRFLVPL.....TDMPTTEVTDIVRENE 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
3	1063	42.1	207	US-09-489-847-320
4	812	32.1	162	US-09-489-847-160
5	586	23.2	114	US-09-489-847-321
6	118.5	4.7	518	US-09-134-001C-4744
7	114.5	4.5	329	US-09-902-540-15354
8	109.5	4.3	610	US-08-970-725-2
9	108.5	4.3	361	US-09-196-520-6
10	104.5	4.1	610	US-08-212-188-2
11	104.5	4.1	610	PCT-US95-02708-2
12	104	4.1	536	US-09-107-532A-5507
13	103	4.1	631	US-09-107-532A-3902
14	103	4.1	1058	US-08-687-289A-5
15	103	4.1	1058	US-09-435-897-5
16	101.5	4.0	677	US-09-543-681A-6388
17	100.5	4.0	413	US-09-540-236-3672
18	100.5	4.0	413	US-10-104-047-3865
19	100	4.0	644	US-09-252-991A-21730
20	99	3.9	563	US-09-949-016-10317
21	99	3.9	584	US-09-693-746-22
22	98.5	3.9	472	US-09-934-899-10
23	98.5	3.9	472	US-09-934-868-30
24	98.5	3.9	472	US-10-701-200-30
25	98.5	3.9	513	US-09-303-518D-582
26	98.5	3.9	516	US-09-252-991A-21329
27	98	3.9	534	US-09-328-352-6713
28	98	3.9	619	US-09-540-236-2377
29	96.5	3.8	509	US-09-252-991A-30864
30	96.5	3.8	513	US-09-303-518D-580
31	96.5	3.8	96.5	Sequence 320, App
32	96.5	3.8	96.5	Sequence 160, App
33	96.5	3.8	96.5	Sequence 321, App
34	96.5	3.8	96.5	Sequence 4744, App
35	96.5	3.8	96.5	Sequence 15354, A
36	96.5	3.8	96.5	Sequence 2, Appl
37	95.5	3.7	95.5	Sequence 6, Appl
38	95	3.7	95	Sequence 2, Appl
39	95	3.7	95	Sequence 5507, App
40	94.5	3.7	94.5	Sequence 3902, App
41	94	3.7	94	Sequence 5, Appl
42	94	3.7	94	Sequence 5, Appl
43	94	3.7	94	Sequence 6388, App
44	93.5	3.7	93.5	Sequence 3672, App
45	93.5	3.7	93.5	Sequence 3865, App
46	93.5	3.7	93.5	Sequence 21730, A
47	93.5	3.7	93.5	Sequence 10317, A
48	93.5	3.7	93.5	Sequence 22, Appl
49	93	3.7	93	Sequence 10, Appl
50	93	3.7	93	Sequence 30, Appl
51	93	3.7	93	Sequence 30, Appl
52	92.5	3.7	92.5	Sequence 582, App
53	92.5	3.7	92.5	Sequence 21329, A
54	92.5	3.7	92.5	Sequence 6713, App
55	92	3.6	92	Sequence 2377, App
56	92	3.6	92	Sequence 30864, A
57	92	3.6	92	Sequence 580, App
58	91.5	3.6	91.5	Sequence 320, App
59	91.5	3.6	91.5	Sequence 160, App
60	91.5	3.6	91.5	Sequence 321, App
61	91.5	3.6	91.5	Sequence 4744, App
62	91.5	3.6	91.5	Sequence 15354, A
63	91.5	3.6	91.5	Sequence 2, Appl
64	91	3.6	91	Sequence 6, Appl
65	91	3.6	91	Sequence 2, Appl
66	91	3.6	91	Sequence 5507, App
67	91	3.6	91	Sequence 3902, App
68	91	3.6	91	Sequence 5, Appl
69	91	3.6	91	Sequence 5, Appl
70	91	3.6	91	Sequence 6388, App
71	90.5	3.6	90.5	Sequence 3672, App
72	90.5	3.6	90.5	Sequence 3865, App
73	90.5	3.6	90.5	Sequence 21730, A
74	90.5	3.6	90.5	Sequence 10317, A
75	90.5	3.6	90.5	Sequence 22, Appl
76	90.5	3.6	90.5	Sequence 10, Appl
77	90	3.6	90	Sequence 30, Appl
78	90	3.6	90	Sequence 30, Appl
79	90	3.6	90	Sequence 582, App
80	90	3.6	90	Sequence 21329, A
81	89.5	3.5	89.5	Sequence 6713, App
82	89.5	3.5	89.5	Sequence 2377, App
83	89.5	3.5	89.5	Sequence 30864, A
84	89.5	3.5	89.5	Sequence 580, App
85	89.5	3.5	89.5	Sequence 320, App
86	89.5	3.5	89.5	Sequence 160, App
87	89.5	3.5	89.5	Sequence 321, App
88	89.5	3.5	89.5	Sequence 4744, App
89	89.5	3.5	89.5	Sequence 15354, A
90	89.5	3.5	89.5	Sequence 2, Appl
91	89	3.5	89	Sequence 6, Appl
92	89	3.5	89	Sequence 2, Appl
93	89	3.5	89	Sequence 5507, App
94	88.5	3.5	88.5	Sequence 3902, App
95	88.5	3.5	88.5	Sequence 5, Appl
96	88.5	3.5	88.5	Sequence 5, Appl
97	88.5	3.5	88.5	Sequence 6388, App
98	88.5	3.5	88.5	Sequence 3672, App
99	88.5	3.5	88.5	Sequence 3865, App
100	88.5	3.5	88.5	Sequence 21730, A
101	88.5	3.5	88.5	Sequence 10317, A
102	88	3.5	88	Sequence 22, Appl
103	88	3.5	88	Sequence 10, Appl

Sequence 21, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 3105, App
Sequence 7942, App
Sequence 7, Appl
Sequence 8, Appl
Sequence 12897, A
Sequence 12897, A
Sequence 2020, App
Sequence 14, Appl
Sequence 74, Appl
Sequence 28134, A
Sequence 3, Appl
Sequence 9, Appl
Sequence 348, App
Sequence 8414, App
Sequence 16765, A
Sequence 7512, App
Sequence 11844, A
Sequence 3486, App
Sequence 31637, A
Sequence 14, Appl
Sequence 12781, A
Sequence 12877, A
Sequence 34, Appl
Sequence 34, Appl
Sequence 4234, App
Sequence 10467, A
Sequence 8, Appl
Sequence 7659, App
Sequence 3651, App
Sequence 5001, App
Sequence 27411, A
Sequence 305, App
Sequence 443, App
Sequence 426, App
Sequence 10085, A
Sequence 19270, A
Sequence 52, Appl
Sequence 11138, A
Sequence 5694, App
Sequence 4534, App
Sequence 2206, App
Sequence 11, Appl
Sequence 18036, A
Sequence 3, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 16824, A
Sequence 499, App
Sequence 3842, App
Sequence 3722, App
Sequence 16249, A
Sequence 626, App
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 6643, App
Sequence 23726, A
Sequence 10560, A
Sequence 2977, App
Sequence 4956, App
Sequence 19033, A
Sequence 4006, App
Sequence 5459, App
Sequence 1, Appl
Sequence 93, Appl
Sequence 180, App
Sequence 5305, App
Sequence 9805, App

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 23:20:36 ; Search time 71 Seconds

(without alignments)

2895.381 Million cell updates/sec

Perfect score: 2527

Sequence: 1 MVKPPALHYWPLRLVPL.....TDMPTTEVTDIVENRENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA_Main:

1: /cgn2_6/protdata1/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/protdata1/pubpaa/US08_PUBCOMB.pep.*

3: /cgn2_6/protdata1/pubpaa/US09_PUBCOMB.pep.*

4: /cgn2_6/protdata1/pubpaa/US10A_PUBCOMB.pep.*

5: /cgn2_6/protdata1/pubpaa/US10B_PUBCOMB.pep.*

6: /cgn2_6/protdata1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
35	2527	100.0	492	4	US-10-167-749-7
45	2527	100.0	492	4	US-10-210-951-16
47	2527	100.0	492	4	US-10-211-884-16
73	2527	100.0	492	4	US-10-170-481A-7
75	2527	100.0	492	4	US-10-210-028-7
80	2527	100.0	492	4	US-10-162-521A-7
81	2527	100.0	492	4	US-10-211-858-16
93	2527	100.0	492	5	US-10-918-851-7
94	2527	100.0	492	5	US-10-805-667-7
95	2527	100.0	492	5	US-10-897-359-7
96	2527	100.0	492	5	US-10-893-802-7
97	2527	100.0	492	5	US-10-897-360-7
98	2527	100.0	492	5	US-10-367-057-48
100	2527	100.0	492	6	US-11-129-762-7
101	2522	99.8	492	5	US-10-169-596A-2
102	2522	99.8	492	5	US-10-489-125B-3
103	2522	99.0	492	5	US-10-169-596A-16
104	2285	90.4	445	4	US-10-839-882-8
105	1396.5	55.3	306	5	US-10-450-763-40695
106	1162	46.0	459	5	US-10-450-763-40696
107	1063	42.1	207	4	US-10-351-334-320
108	1049	41.5	205	4	US-10-264-237-2326
109	812	32.1	161	5	US-10-472-533-388
110	812	32.1	162	4	US-10-351-334-160
111	586	23.2	114	4	US-10-351-334-321
112	256	10.1	47	3	US-09-864-761-40397
113	193	7.6	40	3	US-09-864-761-41066
114	122.5	4.8	512	4	US-10-161-493-36

115	118.5	4.7	518	4	US-10-724-972A-6261	Sequence 6261, Ap
116	111	4.4	556	5	US-10-474-792-242	Sequence 242, App
117	109.5	4.3	522	4	US-10-425-115-327280	Sequence 327280, A
118	108.5	4.3	361	4	US-10-424-599-147020	Sequence 147020, A
119	108.5	4.3	492	4	US-10-282-122A-76094	Sequence 76094, A
120	108	4.3	533	4	US-10-214-867A-9	Sequence 9, Appli
121	108	4.3	740	4	US-10-282-122A-75847	Sequence 75847, A
122	108	4.3	751	3	US-09-815-242-14001	Sequence 14001, A
123	107	4.2	466	4	US-10-437-963-159111	Sequence 159111, A
124	106	4.2	466	4	US-10-282-122A-53222	Sequence 53222, A
125	105.5	4.2	711	4	US-10-369-493-3168	Sequence 3168, Ap
126	105.5	4.2	1230	4	US-10-156-761-14097	Sequence 14097, A
127	105	4.2	499	4	US-10-425-114-40938	Sequence 40938, A
128	105	4.2	1019	4	US-10-425-114-42517	Sequence 42517, A
129	105	4.2	1019	4	US-10-335-977-5444	Sequence 5444, Ap
130	104.5	4.1	447	5	US-10-474-792-502	Sequence 502, App
131	104.5	4.1	467	4	US-10-282-122A-66783	Sequence 66783, A
132	104	4.1	548	4	US-10-282-122A-57565	Sequence 57565, A
133	103.5	4.1	398	4	US-10-282-122A-58458	Sequence 58458, A
134	103.5	4.1	551	4	US-10-127-032-125	Sequence 125, App
135	103.5	4.1	551	4	US-10-389-647-689	Sequence 689, App
136	103.5	4.1	840	5	US-10-502-667-1	Sequence 1, Appli
137	103.5	4.1	1061	4	US-10-415-934-9	Sequence 9, Appli
138	103.5	4.1	1061	6	US-11-097-143-23451	Sequence 23451, A
139	103	4.1	207	4	US-10-424-599-192311	Sequence 192311, A
140	103	4.1	1058	4	US-10-300-473-5	Sequence 5, Appli
141	103	4.1	1058	5	US-10-967-091-26	Sequence 26, Appli
142	103	4.1	1210	4	US-10-128-714-3078	Sequence 3078, Ap
143	103	4.1	1246	4	US-10-128-714-8078	Sequence 8078, Ap
144	102.5	4.1	526	5	US-10-501-282-1586	Sequence 1586, Ap
145	102.5	4.1	553	5	US-10-501-282-1588	Sequence 1588, Ap
146	102.5	4.1	559	5	US-10-501-282-1590	Sequence 1590, Ap
147	102.5	4.1	566	3	US-09-971-361-7	Sequence 7, Appli
148	102.5	4.1	566	6	US-11-108-870-7	Sequence 7, Appli
149	102.5	4.1	853	4	US-10-156-761-11724	Sequence 11724, A
150	102	4.0	1019	2	US-08-834-705-18	Sequence 18, Appli
151	102	4.0	1020	3	US-09-882-227-188	Sequence 188, App
152	101.5	4.0	960	4	US-10-282-122A-61140	Sequence 61140, A
153	101	4.0	360	4	US-10-424-599-277493	Sequence 277493, A
154	101	4.0	377	4	US-10-425-114-44189	Sequence 44189, A
155	101	4.0	446	4	US-10-282-122A-77258	Sequence 77258, A
156	101	4.0	623	4	US-10-425-115-193134	Sequence 193134, A
157	101	4.0	664	4	US-10-416-898-6	Sequence 6, Appli
158	100.5	4.0	406	4	US-10-627-124-4	Sequence 4, Appli
159	100.5	4.0	450	5	US-10-732-923-23795	Sequence 23795, A
160	100.5	4.0	461	4	US-10-104-047-3665	Sequence 3665, Ap
161	100.5	4.0	555	4	US-10-282-122A-72304	Sequence 72304, A
162	100	4.0	326	5	US-10-501-282-5142	Sequence 5140, Ap
163	100	4.0	327	5	US-10-501-282-5142	Sequence 5142, Ap
164	100	4.0	487	4	US-10-369-493-12592	Sequence 12592, A
165	100	4.0	557	4	US-10-437-963-201648	Sequence 201648, A
166	100	4.0	597	4	US-10-369-493-12700	Sequence 12700, A
167	100	4.0	880	4	US-10-436-715-31	Sequence 31, Appli
168	100	4.0	880	4	US-10-436-715-81	Sequence 81, Appli
169	99.5	3.9	402	4	US-10-282-122A-66605	Sequence 66605, A
170	99.5	3.9	534	4	US-10-282-122A-77170	Sequence 77170, A
171	99	3.9	519	4	US-10-409-701-19	Sequence 19, Appli
172	99	3.9	535	4	US-10-163-866-43	Sequence 43, Appli
173	99	3.9	535	4	US-10-163-866-44	Sequence 44, Appli
174	99	3.9	584	4	US-10-283-423-22	Sequence 22, Appli
175	99	3.9	584	4	US-10-213-821-22	Sequence 22, Appli
176	99	3.9	584	4	US-10-736-048-22	Sequence 22, Appli
177	99	3.9	584	5	US-10-489-425-16	Sequence 16, Appli
178	98.5	3.9	472	3	US-09-934-899-10	Sequence 10, Appli
179	98.5	3.9	472	3	US-09-934-868-30	Sequence 30, Appli
180	98.5	3.9	472	4	US-10-353-457-10	Sequence 10, Appli
181	98.5	3.9	472	4	US-10-353-456-10	Sequence 10, Appli
182	98.5	3.9	603	4	US-10-701-200-30	Sequence 30, Appli
183	98.5	3.9	641	4	US-10-424-599-164022	Sequence 164022, A
184	98.5	3.9	641	4	US-10-072-012-246	Sequence 246, App
185	98	3.9	398	4	US-10-369-493-9888	Sequence 9888, Ap
186	98	3.9	434	4	US-10-369-493-9916	Sequence 9916, Ap
187	98	3.9	537	4	US-10-282-122A-60383	Sequence 60383, A

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2005, 23:20:47 ; Search time 7 Seconds
(without alignments)
336.551 Million cell updates/sec

Perfect score: 2527

Sequence: 1 MVKFPALTHYKPLRELVLPL.....TDMPTREVTIVREBENE 492

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 26661 seqs, 4788334 residues

Total number of hits satisfying chosen parameters: 26661

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA New:

- 1: /cgm2_6/ptodata/1/pubaa/US09_NEW_PUB pep.*
- 2: /cgm2_6/ptodata/1/pubaa/US06_NEW_PUB pep.*
- 3: /cgm2_6/ptodata/1/pubaa/US07_NEW_PUB pep.*
- 4: /cgm2_6/ptodata/1/pubaa/US08_NEW_PUB pep.*
- 5: /cgm2_6/ptodata/1/pubaa/PCT_NEW_PUB pep.*
- 6: /cgm2_6/ptodata/1/pubaa/US10_NEW_PUB pep.*
- 7: /cgm2_6/ptodata/1/pubaa/US11_NEW_PUB pep.*
- 8: /cgm2_6/ptodata/1/pubaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117.5	4.6	693	6	US-10-467-657-6176
2	99	3.9	563	6	US-10-821-234-1090
3	98.5	3.9	486	6	US-10-467-657-950
4	98	3.9	490	7	US-11-074-176-316
5	98	3.9	495	7	US-11-074-176-60
6	95	3.8	501	7	US-11-055-822-52
7	94.5	3.7	801	6	US-10-793-626-2020
8	90	3.6	431	7	US-11-092-140-6
9	89.5	3.5	984	7	US-11-055-822-508
10	89.5	3.5	984	7	US-11-055-822-594
11	89	3.5	321	6	US-10-467-657-2352
12	89	3.5	674	6	US-10-467-657-6812
13	87.5	3.5	433	7	US-11-082-389-332
14	84	3.3	354	6	US-10-821-234-1618
15	84	3.3	489	6	US-10-858-730-198
16	84	3.3	489	7	US-11-055-822-1152
17	82.5	3.3	342	6	US-10-793-626-2854
18	82.5	3.3	858	7	US-11-077-550-22
19	82.5	3.3	860	7	US-11-077-550-175
20	82.5	3.3	862	7	US-11-077-550-94
21	82.5	3.3	862	7	US-11-077-550-171
22	82.5	3.3	862	7	US-11-077-550-102
23	82.5	3.3	864	7	US-11-077-550-102
24	82.5	3.3	865	7	US-11-077-550-100
25	82.5	3.3	866	7	US-11-077-550-88
26	82.5	3.3	866	7	US-11-077-550-104

27	82.5	3.3	867	7	US-11-077-550-80	Sequence 80, Appl
28	82.5	3.3	867	7	US-11-077-550-96	Sequence 96, Appl
29	82.5	3.3	867	7	US-11-077-550-98	Sequence 98, Appl
30	82.5	3.3	870	7	US-11-077-550-92	Sequence 92, Appl
31	82.5	3.3	871	7	US-11-077-550-84	Sequence 84, Appl
32	82.5	3.3	871	7	US-11-077-550-86	Sequence 86, Appl
33	82.5	3.3	871	7	US-11-077-550-90	Sequence 90, Appl
34	82.5	3.3	876	7	US-11-077-550-82	Sequence 82, Appl
35	82.5	3.3	876	7	US-11-077-550-106	Sequence 106, Appl
36	82.5	3.3	876	7	US-11-077-550-108	Sequence 108, Appl
37	82.5	3.3	888	7	US-11-077-550-112	Sequence 112, Appl
38	82.5	3.3	1070	7	US-11-062	Sequence 4, Appl
39	82.5	3.3	1095	7	US-11-062	Sequence 7, Appl
40	82.5	3.3	1169	7	US-11-077-550-20	Sequence 20, Appl
41	82.5	3.3	1420	7	US-11-077-550-110	Sequence 110, Appl
42	81.5	3.2	205	6	US-10-793-626-2184	Sequence 2184, Ap
43	81	3.2	502	6	US-10-467-657-7332	Sequence 7332, Ap
44	80.5	3.2	372	6	US-10-467-657-590	Sequence 590, Appl
45	80	3.2	842	6	US-10-645-441-2	Sequence 2, Appl
46	79.5	3.1	360	6	US-10-858-730-110	Sequence 110, Appl
47	79.5	3.1	391	7	US-11-082-389-172	Sequence 172, Appl
48	79	3.1	196	6	US-10-485-517-420	Sequence 420, Appl
49	78.5	3.1	291	6	US-10-467-657-3890	Sequence 3890, Ap
50	78.5	3.1	322	7	US-11-082-389-188	Sequence 188, Appl
51	78.5	3.1	363	6	US-10-793-626-302	Sequence 302, Appl
52	78.5	3.1	391	7	US-11-082-389-174	Sequence 174, Appl
53	78.5	3.1	539	6	US-10-467-657-3146	Sequence 3146, Ap
54	78	3.1	307	7	US-11-055-822-834	Sequence 834, Appl
55	78	3.1	408	6	US-10-793-626-2286	Sequence 2286, Ap
56	76.5	3.0	393	7	US-11-092-140-2	Sequence 2, Appl
57	76.5	3.0	400	6	US-10-793-626-3116	Sequence 3116, Ap
58	76	3.0	506	6	US-10-485-517-344	Sequence 344, Appl
59	76	3.0	582	6	US-10-793-626-1080	Sequence 1080, Appl
60	75.5	3.0	540	6	US-10-485-517-223	Sequence 223, Appl
61	75.5	3.0	639	7	US-11-074-176-222	Sequence 222, Appl
62	75.5	3.0	637	7	US-11-082-389-362	Sequence 362, Appl
63	75	3.0	448	7	US-11-055-822-826	Sequence 826, Appl
64	75	3.0	455	7	US-11-102-240-4	Sequence 4, Appl
65	75	3.0	538	7	US-11-119-683-1	Sequence 1, Appl
66	75	3.0	1304	6	US-10-821-234-1648	Sequence 1648, Ap
67	74.5	2.9	394	6	US-10-392-234A-46	Sequence 46, Appl
68	74.5	2.9	394	6	US-10-392-234A-52	Sequence 52, Appl
69	74.5	2.9	407	6	US-10-821-234-1389	Sequence 1389, Ap
70	74.5	2.9	464	6	US-10-689-742-164	Sequence 164, Appl
71	74	2.9	368	7	US-11-082-389-320	Sequence 320, Appl
72	74	2.9	506	6	US-10-467-657-2088	Sequence 2088, Ap
73	74	2.9	585	7	US-11-012-762-6	Sequence 6, Appl
74	73.5	2.9	445	6	US-10-793-626-2644	Sequence 2644, Ap
75	73	2.9	340	6	US-11-082-389-14	Sequence 14, Appl
76	73	2.9	450	6	US-10-467-657-2126	Sequence 2126, Ap
77	73	2.9	450	6	US-10-467-657-3124	Sequence 3124, Ap
78	73	2.9	481	6	US-10-467-657-3124	Sequence 3124, Ap
79	73	2.9	481	6	US-10-467-657-6784	Sequence 6784, Ap
80	73	2.9	638	6	US-10-793-626-1468	Sequence 1468, Ap
81	73	2.9	739	7	US-11-082-389-94	Sequence 94, Appl
82	72.5	2.9	534	6	US-10-793-626-920	Sequence 920, Appl
83	72.5	2.9	914	6	US-10-467-657-638	Sequence 638, Appl
84	72	2.8	209	6	US-10-467-657-4066	Sequence 4066, Ap
85	72	2.8	350	6	US-10-502-145-1	Sequence 1, Appl
86	71.5	2.8	336	6	US-10-793-626-624	Sequence 624, Appl
87	71.5	2.8	336	6	US-10-793-626-2600	Sequence 2600, Ap
88	71.5	2.8	447	6	US-10-858-730-107	Sequence 107, Appl
89	71.5	2.8	447	6	US-10-858-730-107	Sequence 107, Appl
90	71.5	2.8	1167	6	US-10-942-072-13	Sequence 13, Appl
91	71	2.8	351	7	US-11-055-822-264	Sequence 264, Appl
92	71	2.8	367	7	US-11-055-822-262	Sequence 262, Appl
93	71	2.8	397	7	US-11-084-508-5	Sequence 5, Appl
94	71	2.8	432	7	US-11-055-822-1096	Sequence 1096, Ap
95	71	2.8	741	6	US-10-793-626-1178	Sequence 1178, Ap
96	71	2.8	741	6	US-10-793-626-1178	Sequence 1178, Ap
97	70.5	2.8	286	6	US-10-858-730-199	Sequence 199, Appl
98	70.5	2.8	291	6	US-10-793-626-2664	Sequence 2664, Ap
99	70.5	2.8	332	6	US-10-793-626-1008	Sequence 1008, Appl
100	70.5	2.8	521	6	US-10-793-626-532	Sequence 532, Appl
101	70.5	2.8	750	6	US-10-689-742-86	Sequence 86, Appl
102	70.5	2.8	928	6	US-10-841-129-4	Sequence 4, Appl